

What is claimed is:

1. A method of performing genetic analysis comprising the steps of:
 - a. scanning genomic DNA or derivatives therefrom from a plurality of individuals, wherein at least 10,000 bases are scanned, for genetic variants;
 - b. identifying said genetic variants in said genomic DNA or derivatives therefrom that occur in a plurality of individuals;
 - c. for at least said genomic variants that occur in a plurality of individuals, but not all of said at least 10,000 bases, scanning genomic DNA or derivatives therefrom from additional individuals to identify which of said genetic variants occur in said additional individuals; and
 - d. based the results of step c), identifying blocks of said variants.
2. A method as recited in claim 1 further comprising the step of using said blocks of variants in an association study, whereby said blocks of variants are associated with a phenotypic trait.
3. The method as recited in claim 2 further comprising the step of diagnosing said phenotypic trait using one or more variants that are in said block.
4. The method as recited in claim 2 further comprising the step of using said variants associated with a phenotypic trait to identify a potential drug target.
5. The method as recited in claim 4 further comprising the step of using said potential drug target in a small molecule screening process.
6. The method as recited in claim 1 wherein said step of scanning genomic DNA or derivatives therefrom comprises the steps of:
 - a. forming an array of probes a) complementary to portions of a first sequence of said genomic DNA or derivative therefrom and b) complementary to variants of said genomic DNA or derivative therefrom;
 - b. hybridizing said genomic DNA or derivative therefrom to said array; and

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- c. identifying where said genomic DNA or derivative therefrom hybridize to said array.
 - 7. A method as recited in claim 1 wherein said step of scanning genomic DNA comprises the step of sequencing said genomic DNA with a gel based sequencer.
 - 5 8. The method as recited in claim 1 wherein said step of scanning genomic DNA comprises the step of sequencing said genomic DNA with a capillary based sequencer.
 - 9. The method as recited in claim 1 wherein only variants that occur in more than 10% of the said plurality of individuals are used in step c).
 - 10. The method as recited in claim 1 where said step of scanning genomic DNA to identify which is said variants occur in additional individuals comprises the steps of:
 - a. exposing labeled genomic DNA or a derivative thereof to a high density array of probes complementary to said variants; and
 - b. determining where said genomic DNA hybridizes to said high density array.
 - 15 11. The method as recited in claim 1 where said step of scanning genetic DNA to identify which is said variants occur in additional individuals comprises the use of an Invader assay.
 - 20 12. The method as recited in claim 1 where said step of scanning genetic DNA to identify which is said variants occur in additional individuals comprises the use of a Taqman assay.
 - 13. The method as recited in claim 1 wherein more than 1×10^6 bases are scanned for variants.
 - 25 14. The method as recited in claim 1 wherein more than 1×10^7 bases are scanned for variants.
 - 15. The method as recited in claim 1 wherein more than 1×10^8 bases are scanned for variants.

16. The method as recited in claim 1 wherein more than 1×10^9 bases are scanned for variants.
 17. The method as recited in claim 1 wherein introns are scanned for variants.
 18. The method as recited in claim 1 wherein introns and exons are scanned for variants.
 19. The method as recited in claim 1 wherein more than 10% of all the non-repeat genomic DNA from the organism is scanned for variants.
 20. The method as recited in claim 1 wherein more than 25% of all the non-repeat genomic DNA from an organism is scanned for variants.
 21. The method as recited in claim 1 wherein more than 50% of all the non-repeat genomic DNA from an organism is scanned for variants.
 22. The method as recited in claim 1 wherein more than 75% of all the non-repeat genomic DNA from an organism is scanned for variants.
 23. The method as recited in claim 1 wherein said variants are single nucleotide polymorphisms.
 24. The method as recited in claim 2 further comprising the step of using the results of the association study to stratify a patent population in a clinical trial.
 25. The method as recited in claim 2 further comprising the step of using the results of the association study to stratify patents that respond to a drug from those who do not respond to a drug.
 26. The method as recited in claim 2 further comprising the step of using the results of the association study to stratify patents that will show toxic response to a drug from patents that will not show toxic response to a drug.